SEQUENCE LISTING

SEQ ID 1 – NadA from strain 2996, with C-terminus deletion

MKHFPSKVLTTAILATFCSGALAATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAADVEADDF
KGLGLKKVVTNLTKTVNENKQNVDAKVKAAESEIEKLTTKLADTDAALADTDAALDATTNALNKLGENITTFAEETKTNIV
KIDEKLEAVADTVDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAEEETKQNVDAKVKAAETAAGKAEAAAGTANTAAD
KAEAVAAKVTDIKADIATNKDNIAKKANSADVYTREESDSKFVRIDGLNATTEKLDTRLASAEKSIADHDTRLNGLDKTVS
DLRKETRQGLAEQAALSGLFQPYNVG

SEQ ID 2 – NadA from strain 2996, with C-terminus deletion and leader peptide processed

ATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAADVEADDFKGLGLKKVVTNLTKTVNENKQNV
DAKVKAAESEIEKLTTKLADTDAALADTDAALDATTNALNKLGENITTFAEETKTNIVKIDEKLEAVADTVDKHAEAFNDI
ADSLDETNTKADEAVKTANEAKQTAEEETKQNVDAKVKAAETAAGKAEAAAGTANTAADKAEAVAAKVTDIKADIATNKDNI
AKKANSADVYTREESDSKFVRIDGLNATTEKLDTRLASAEKSIADHDTRLNGLDKTVSDLRKETRQGLAEQAALSGLFQPY
NVG

SEQ ID 3 – ΔG741 from MC58 strain

VAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAAQGAEKTYGNGDSLNTGKLKNDKVSRFDFIRQIEVDGQL
ITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDAGGKLTYT
IDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEKGSYSLGIFGGKAQEVAGSAEVKTVNGIRHIG
LAAKQ

SEQ ID 4 – 936 from MC58 strain with leader peptide processed

VSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETTARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQ
IARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQITQKVST
TVGVQKVITLYQNYVQR

SEQ ID 5 – 953 from MC58 strain with leader peptide processed

ATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIR
FVSTKFNFNGKKLVSVDGNLTMHGKTAPVKLKAEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDIQ
IEAAKQ

SEQ ID 6 – ΔG287 from MC58 strain

SPDVKSADTLSKPAAPVVSEKETEAKEDAPQAGSQGQGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNDMPQN
AAGTDSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDDPSAGGQNAGNTAAQGANQAGNNQAAGSSD
PIPASNPAPANGGSNFGRVDLANGVLIDGPSQNITLTHCKGDSCSGNNFLDEEVQLKSEFEKLSDADKISNYKKDGKNDKF
VGLVADSVQMKGINQYIIFYKPKPTSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYL
TYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVDGIIDSGDDLHMGTQKF
KAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGGFGVFAGKKEQD

SEQ ID 7 – 287-953 hybrid

MASPDVKSADTLSKPAAPVVSEKETEAKEDAPQAGSQGQGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMP
QNAADTDSLTPNHTPASNMPAGNMENQAPDAGESEQPANQPDMANTADGMQGDDPSAGGENAGNTAAQGTNQAENNQTAGS
QNPASSTNPSATNSGGDFGRTNVGNSVVIDGPSQNITLTHCKGDSCSGNNFLDEEVQLKSEFEKLSDADKISNYKKDGKND
GKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPE
GNYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPSRGRFAAKVDFGSKSVDGIIDSGDGLH
MGTQKFKAAIDGNGFKGTWTENGGGDVSGKFYGPAGEEVAGKYSYRPTDAEKGGFGVFAGKKEQDGSGGGGATYKVDEYHA
NARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNG
KKLVSVDGNLTMHGKTAPVKLKAEKFNCYQSPMAKTEVCGGDFSTTIDRTKWGVDYLVNVGMTKSVRIDIQIEAAKQ*

SEQ ID 8 – 936-741 hybrid

MVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETTARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVG
QIARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQITQKVS

TTVGVQKVITLYQNYVQRGSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAAQGAEKTYGNGDSLN
TGKLKNDKVSRFDFIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLP
EGGRATYRGTAFGSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEKGSYSLGI
FGGKAQEVAGSAEVKTVNGIRHIGLAAKQ*

5 ***SEQ ID 9 – linker***

GSGGGG

SEQ ID 10 – 741 sequence

CSSGGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAAQGAEKTYGNGDSLNTGKLKNDKVSRFDFIRQ
IEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDA
10 GGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEKGSYSLGIFGGKAQEVAGSAEVKTV
NGIRHIGLAAKQ

SEQ ID 11 – 741 sequence

CSSGGGGGVAADIGAGLADALTAPLDHKDKSLQSLTLDQSVRKNEKLKLAAQGAEKTYGNGDSLNTGKLKNDKVSRFDFIRQ
IEVDGQLITLESGEFQIYKQDHSAVVALQIEKINNPDKIDSLINQRSFLVSGLGGEHTAFNQLPDGKAEYHGKAFSSDDAG
15 GKLTYTIDFAAKQGHGKIEHLKTPEQNVELAAAELKADEKSHAVILGDTRYGSEEKGTYHLALFGDRAQEIAGSATVKIGE
KVHEIGIAGKQ

SEQ ID 12 – 741 sequence

CSSGGGGGSGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEDSIPQNGTLTLSAQGAEKTFKAGDKDNSLNTGKLKNDKI
SRFDFVQKIEVDGQTITLASGEFQIYKQNHSAVVALQIEKINNPDKTDSLINQRSFLVSGLGGEHTAFNQLPGGKAEYHGK
20 AFSSDDPNGRLHYSIDFTKKQGYGRIEHLKTLEQNVELAAAELKADEKSHAVILGDTRYGSEEKGTYHLALFGDRAQEIAG
SATVKIGEKVHEIGIAGKQ